

SEQUENCE LISTING

<110> Okano, Shinji
 Yonemitsu, Yoshikazu
 Sueishi, Katsuo
 Shibata, Satoko
 Hasegawa, Mamoru

<120> Method for Producing Gene Transferred Dendritic Cells

<130> 50026/058001

<140> US 10/578,085
 <141> 2006-05-03

<150> PCT/JP2004/016089
 <151> 2004-10-29

<150> JP 2004-187028
 <151> 2004-06-24

<150> JP 2003-374808
 <151> 2003-11-04

<160> 15

<170> PatentIn version 3.3

<210> 1
 <211> 10
 <212> DNA
 <213> Artificial

<220>
 <223> artificially synthesized sequence

<400> 1
 ctttcaccct 10

<210> 2
 <211> 15
 <212> DNA
 <213> Artificial

<220>
 <223> artificially synthesized sequence

<400> 2
 tttttcttac tacgg 15

<210> 3
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> artificially synthesized sequence

 <400> 3
 cggccgcaga tcttcacg 18

 <210> 4
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <223> artificially synthesized sequence

 <400> 4
 atgcatgccg gcagatga 18

 <210> 5
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <223> artificially synthesized sequence

 <400> 5
 gttgagtact gcaagagc 18

 <210> 6
 <211> 42
 <212> DNA
 <213> Artificial

 <220>
 <223> artificially synthesized sequence

 <400> 6
 tttgccggca tgcattgttc ccaaggggag agttttgcaa cc 42

 <210> 7
 <211> 18
 <212> DNA
 <213> Artificial

 <220>
 <223> artificially synthesized sequence

 <400> 7
 atgcatgccg gcagatga 18

 <210> 8
 <211> 21

<212> DNA
<213> Artificial

<220>
<223> artificially synthesized sequence

<400> 8
tgggtgaatg agagaatcag c

21

<210> 9
<211> 10
<212> PRT
<213> Artificial

<220>
<223> an artificially synthesized peptide

<400> 9

Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

<210> 10
<211> 10
<212> PRT
<213> Artificial

<220>
<223> an artificially synthesized peptide

<400> 10

Glu Leu Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

<210> 11
<211> 9
<212> PRT
<213> Artificial

<220>
<223> an artificially synthesized peptide

<400> 11

Gly Ile Leu Gly Phe Val Phe Thr Leu
1 5

<210> 12
<211> 561
<212> DNA
<213> Homo sapiens

```

<220>
<221> CDS
<222> (1)..(561)

<220>
<221> sig_peptide
<222> (1)..(21)

<400> 12
atg acc aac aag tgt ctc ctc caa att gct ctc ctg ttg tgc ttc tcc      48
Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
1          5          10          15

act aca gct ctt tcc atg agc tac aac ttg ctt gga ttc cta caa aga      96
Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
          20          25          30

agc agc aat ttt cag tgt cag aag ctc ctg tgg caa ttg aat ggg agg      144
Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
          35          40          45

ctt gaa tat tgc ctc aag gac agg atg aac ttt gac atc cct gag gag      192
Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
          50          55          60

att aag cag ctg cag cag ttc cag aag gag gac gcc gca ttg acc atc      240
Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
65          70          75          80

tat gag atg ctc cag aac atc ttt gct att ttc aga caa gat tca tct      288
Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
          85          90          95

agc act ggc tgg aat gag act att gtt gag aac ctc ctg gct aat gtc      336
Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
          100          105          110

tat cat cag ata aac cat ctg aag aca gtc ctg gaa gaa aaa ctg gag      384
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
          115          120          125

aaa gaa gat ttt acc agg gga aaa ctc atg agc agt ctg cac ctg aaa      432
Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
          130          135          140

aga tat tat ggg agg att ctg cat tac ctg aag gcc aag gag tac agt      480
Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
145          150          155          160

cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg aac ttt tac      528
His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
          165          170          175

ttc att aac aga ctt aca ggt tac ctc cga aac      561
Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
          180          185

```

<210> 13
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 13

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
 1 5 10 15

Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
 20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
 145 150 155 160

His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
 165 170 175

Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 180 185

<210> 14
 <211> 546
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(546)

<220>
 <221> sig_peptide
 <222> (1)..(21)

<400> 14
 atg aac aac agg tgg atc ctc cac gct gcg ttc ctg ctg tgc ttc tcc 48
 Met Asn Asn Arg Trp Ile Leu His Ala Ala Phe Leu Leu Cys Phe Ser
 1 5 10 15

acc aca gcc ctc tcc atc aac tat aag cag ctc cag ctc caa gaa agg 96
 Thr Thr Ala Leu Ser Ile Asn Tyr Lys Gln Leu Gln Leu Gln Glu Arg
 20 25 30

acg aac att cgg aaa tgt cag gag ctc ctg gag cag ctg aat gga aag 144
 Thr Asn Ile Arg Lys Cys Gln Glu Leu Leu Glu Gln Leu Asn Gly Lys
 35 40 45

atc aac ctc acc tac agg gcg gac ttc aag atc cct atg gag atg acg 192
 Ile Asn Leu Thr Tyr Arg Ala Asp Phe Lys Ile Pro Met Glu Met Thr
 50 55 60

gag aag atg cag aag agt tac act gcc ttt gcc atc caa gag atg ctc 240
 Glu Lys Met Gln Lys Ser Tyr Thr Ala Phe Ala Ile Gln Glu Met Leu
 65 70 75 80

cag aat gtc ttt ctt gtc ttc aga aac aat ttc tcc agc act ggg tgg 288
 Gln Asn Val Phe Leu Val Phe Arg Asn Asn Phe Ser Ser Thr Gly Trp
 85 90 95

aat gag act att gtt gta cgt ctc ctg gat gaa ctc cac cag cag aca 336
 Asn Glu Thr Ile Val Val Arg Leu Leu Asp Glu Leu His Gln Gln Thr
 100 105 110

gtg ttt ctg aag aca gta cta gag gaa aag caa gag gaa aga ttg acg 384
 Val Phe Leu Lys Thr Val Leu Glu Glu Lys Gln Glu Glu Arg Leu Thr
 115 120 125

tgg gag atg tcc tca act gct ctc cac ttg aag agc tat tac tgg agg 432
 Trp Glu Met Ser Ser Thr Ala Leu His Leu Lys Ser Tyr Tyr Trp Arg
 130 135 140

gtg caa agg tac ctt aaa ctc atg aag tac aac agc tac gcc tgg atg 480
 Val Gln Arg Tyr Leu Lys Leu Met Lys Tyr Asn Ser Tyr Ala Trp Met
 145 150 155 160

gtg gtc cga gca gag atc ttc agg aac ttt ctc atc att cga aga ctt 528
 Val Val Arg Ala Glu Ile Phe Arg Asn Phe Leu Ile Ile Arg Arg Leu

165 170 175
 acc aga aac ttc caa aac 546
 Thr Arg Asn Phe Gln Asn
 180

 <210> 15
 <211> 182
 <212> PRT
 <213> Mus musculus

 <400> 15
 Met Asn Asn Arg Trp Ile Leu His Ala Ala Phe Leu Leu Cys Phe Ser
 1 5 10 15

 Thr Thr Ala Leu Ser Ile Asn Tyr Lys Gln Leu Gln Leu Gln Glu Arg
 20 25 30

 Thr Asn Ile Arg Lys Cys Gln Glu Leu Leu Glu Gln Leu Asn Gly Lys
 35 40 45

 Ile Asn Leu Thr Tyr Arg Ala Asp Phe Lys Ile Pro Met Glu Met Thr
 50 55 60

 Glu Lys Met Gln Lys Ser Tyr Thr Ala Phe Ala Ile Gln Glu Met Leu
 65 70 75 80

 Gln Asn Val Phe Leu Val Phe Arg Asn Asn Phe Ser Ser Thr Gly Trp
 85 90 95

 Asn Glu Thr Ile Val Val Arg Leu Leu Asp Glu Leu His Gln Gln Thr
 100 105 110

 Val Phe Leu Lys Thr Val Leu Glu Glu Lys Gln Glu Glu Arg Leu Thr
 115 120 125

 Trp Glu Met Ser Ser Thr Ala Leu His Leu Lys Ser Tyr Tyr Trp Arg
 130 135 140

 Val Gln Arg Tyr Leu Lys Leu Met Lys Tyr Asn Ser Tyr Ala Trp Met
 145 150 155 160

 Val Val Arg Ala Glu Ile Phe Arg Asn Phe Leu Ile Ile Arg Arg Leu
 165 170 175

Thr Arg Asn Phe Gln Asn
180